



217770US0PCT.ST25
SEQUENCE LISTING

10 Rec'd PCT

28 JUL 2004

<110> SHIBATA, TAKASHI
NOGUCHI, YUJI
YAMASHITA, MICHIO

<120> GENE ENCODING CYCLIC LIPOPEPTIDE ACYLASE AND EXPRESSION OF THE
SAME

<130> 217770US0PCT

<140> 10/019,282

<141> 2002-01-02

<150> PCT/JP00/04285

<151> 2000-06-28

<150> JP189644/1999

<151> 1999-07-02

<160> 76

<170> PatentIn version 3.2

<210> 1

<211> 5692

<212> DNA

<213> Streptomyces Sp.

<220>

<221> CDS

<222> (948)..(3362)

<400> 1
gaattccgga tggttggaga ggccgatcca gacggtgggc ggggcgaaga ggctgtcggc 60
caggccccgct tcgacgaggt cgaagatcga ggcggcgctcc ggaccgtcca ggatggtggt 120
ctccgcgccc accgccagat agggcagcag gaacacgtgc atctgggccg agtggttagag 180
cggcagggag tgcacggggc ggtcggtcgc ggcgaggccg agcgcggtga tcgcgctgac 240
gtactcgtgg accagggccc cgtgcgtcat catcgcgccc ttgggcaggg cgggtggtccc 300
ggaggtgtac agcagctgca ccaggtcgtc ggaggcgggc gggcgccgcg ggggtgaacgc 360
ccgttccgtc tccagggcgt cgagcagcga gccgggcgcg tcgcggagcg cgcgcaccgg 420
gagtcggcg gggagccgc cggcgaggtc cgggtcggtc aggacgagg aggagccgga 480
ctggtcgagg aggtaggcca ggtcgtcgc ggtgaggttc tggttgaccg gtacgtggac 540
gagaccggcc cgtgcgcagg cgaggaagcc gatcagatag gcgtcggagt tgtgcgcgta 600
ggcggccacc cggtcgccgg gggcgagagc gtactcctcg gtgaggacgg cggcggccgt 660
ggagacggcg gcgtccaggg agcggtaggt ccaggtccgg tcggcgtagc gcacggcggt 720
ccggtcgggg gtgcgccggg cgctgcgggt gaggacgccg tcgactgtgc tgctgcgtac 780
acctgtcatg gcgtgatcct gtgcgtccgg gccctcgggg gtcaagaggc tggataccga 840
ccagacgggt gacagcttcc cgggctccct ggctgagtga cgcttggccg tccgggcggt 900
ccggaccggc cgcgcccgtg ccaccggtac cgctgggagg aaacacc ttg acg tta 956
Leu Thr Leu
1

217770US0PCT.ST25

cg	aa	cg	ct	ag	ct	ct	gg	gt	gc	gg	ct	gc	ct	tt	ac	1004
Arg	Asn	Arg	Leu	Arg	Leu	Leu	Gly	Val	Ala	Gly	Leu	Ala	Leu	Phe	Thr	
5						10					15					
gt	tc	gc	tc	ct	cc	cc	gc	ac	gc	tcc	gg	ac	cag	gag	ac	1052
Val	Ser	Ala	Ser	Leu	Pro	Pro	Ala	Thr	Ala	Ser	Gly	Thr	Gln	Glu	Thr	
20					25					30					35	
cg	ca	cc	tcc	gg	ag	gg	ctt	tc	gc	gt	at	cg	ta	ac	gag	1100
Arg	His	Pro	Ser	Gly	Ser	Gly	Leu	Ser	Ala	Val	Ile	Arg	Tyr	Thr	Glu	
				40					45					50		
ta	gg	att	cc	ca	at	gt	gc	gag	gac	ta	gc	cag	tt	gg	tt	1148
Tyr	Gly	Ile	Pro	His	Ile	Val	Ala	Glu	Asp	Tyr	Ala	Gln	Leu	Gly	Phe	
			55					60					65			
gg	ac	gg	tgg	gc	cag	gc	gc	gat	cag	gt	tgc	ac	ct	gc	gac	1196
Gly	Thr	Gly	Trp	Ala	Gln	Ala	Ala	Asp	Gln	Val	Cys	Thr	Leu	Ala	Asp	
		70				75					80					
gg	tt	ct	ac	gt	cg	gg	gag	cg	tc	agg	tt	tt	gg	cc	gac	1244
Gly	Phe	Leu	Thr	Val	Arg	Gly	Glu	Arg	Ser	Arg	Phe	Phe	Gly	Pro	Asp	
	85					90					95					
gc	gc	ac	gac	ta	tcc	ct	tcc	tc	gc	gc	ac	aa	ct	tcc	ag	1292
Ala	Ala	Thr	Asp	Tyr	Ser	Leu	Ser	Ser	Ala	Ala	Thr	Asn	Leu	Ser	Ser	
					105					110					115	
ga	ct	ta	tt	cg	gg	gt	cg	ga	ag	gg	ac	gt	gag	aag	ct	1340
Asp	Leu	Tyr	Phe	Arg	Gly	Val	Arg	Asp	Ser	Gly	Thr	Val	Glu	Lys	Leu	
				120				125						130		
ct	aag	gag	ccc	gc	ccc	gc	gg	cc	ag	agg	gac	gt	aag	gag	ac	1388
Leu	Lys	Glu	Pro	Ala	Pro	Ala	Gly	Pro	Ser	Arg	Asp	Val	Lys	Glu	Thr	
			135					140					145			
at	cg	gg	tt	gc	gc	gg	ta	aa	gc	tgg	at	gc	cag	aa	cg	1436
Met	Arg	Gly	Phe	Ala	Ala	Gly	Tyr	Asn	Ala	Trp	Ile	Ala	Gln	Asn	Arg	
		150					155					160				
at	ac	gac	ccc	gc	tgc	cg	gg	gc	tcc	tgg	gt	cg	cc	gt	ac	1484
Ile	Thr	Asp	Pro	Ala	Cys	Arg	Gly	Ala	Ser	Trp	Val	Arg	Pro	Val	Thr	
	165					170					175					
gc	ct	gac	gt	gc	gc	cg	gg	ta	gc	ct	gc	gt	ct	gg	gg	1532
Ala	Leu	Asp	Val	Ala	Ala	Arg	Gly	Tyr	Ala	Leu	Ala	Val	Leu	Gly	Gly	
	180				185					190				195		
ca	gg	cg	gg	at	ga	gg	at	ac	gc	ga	cag	cc	cc	ac	gc	1580
Gln	Gly	Arg	Gly	Ile	Asp	Gly	Ile	Thr	Ala	Ala	Gln	Pro	Pro	Thr	Ala	
				200				205						210		
gt	cct	cc	gc	gc	gg	gt	ac	ccc	gag	gag	gc	gc	ac	gc	gc	1628
Ala	Pro	Pro	Ala	Ala	Gly	Val	Thr	Pro	Glu	Glu	Ala	Ala	Thr	Ala	Ala	
			215					220					225			
gag	cg	ct	ct	tc	ac	cag	aa	gc	gac	at	gg	tcc	aa	gc	gt	1676
Glu	Arg	Leu	Leu	Ser	Thr	Gln	Asn	Ala	Asp	Met	Gly	Ser	Asn	Ala	Val	
		230					235					240				
gc	tt	gac	gg	tcc	ac	ac	gt	aa	gg	cg	gg	ct	tt	ct	gg	1724
Ala	Phe	Asp	Gly	Ser	Thr	Thr	Val	Asn	Gly	Arg	Gly	Leu	Leu	Leu	Gly	
	245					250					255					
aa	cc	ca	ta	cc	tgg	cag	gg	ga	cg	cg	tt	tgg	cag	gc	cag	1772
Asn	Pro	His	Tyr	Pro	Trp	Gln	Gly	Gly	Arg	Arg	Phe	Trp	Gln	Ala	Gln	
					265					270					275	

217770US0PCT.ST25

cag	acg	atc	ccc	ggc	gag	ctg	aac	gtg	tcg	ggc	gcg	tcc	ctg	ctg	ggc	1820
Gln	Thr	Ile	Pro	Gly	Glu	Leu	Asn	Val	Ser	Gly	Ala	Ser	Leu	Leu	Gly	
				280					285					290		
gcg	acg	acg	atc	tcg	atc	ggg	cac	aac	gcc	gat	gtg	gcg	tgg	agc	cat	1868
Ala	Thr	Thr	Ile	Ser	Ile	Gly	His	Asn	Ala	Asp	Val	Ala	Trp	Ser	His	
			295					300					305			
acg	gtc	gcc	acg	ggc	gtc	acg	ctg	aat	ctg	cat	cag	ctc	agc	ctc	gat	1916
Thr	Val	Ala	Thr	Gly	Val	Thr	Leu	Asn	Leu	His	Gln	Leu	Ser	Leu	Asp	
		310					315					320				
ccg	gcc	gac	ccg	acc	gtc	tat	ctg	gtg	gac	ggg	aag	cgg	gag	cgg	atg	1964
Pro	Ala	Asp	Pro	Thr	Val	Tyr	Leu	Val	Asp	Gly	Lys	Arg	Glu	Arg	Met	
	325					330					335					
acg	cag	cgg	acg	gtg	agc	gtc	ccg	gtg	aag	ggc	ggg	gcc	gac	gtg	acc	2012
Thr	Gln	Arg	Thr	Val	Ser	Val	Pro	Val	Lys	Gly	Gly	Ala	Asp	Val	Thr	
340					345					350					355	
cgc	acc	cag	tgg	tgg	acc	cgc	tac	ggg	ccg	gtg	gcc	acc	tcg	atg	ggc	2060
Arg	Thr	Gln	Trp	Trp	Thr	Arg	Tyr	Gly	Pro	Val	Ala	Thr	Ser	Met	Gly	
				360					365					370		
gcg	ggg	ctg	ccg	ttg	ccg	tgg	acg	gcg	agc	acg	gcg	tac	gcg	ctg	aac	2108
Ala	Gly	Leu	Pro	Leu	Pro	Trp	Thr	Ala	Ser	Thr	Ala	Tyr	Ala	Leu	Asn	
			375					380					385			
gat	ccg	aac	gcg	acg	aat	ctg	cgg	atg	gcg	gac	acc	ggt	ctg	ggc	ttc	2156
Asp	Pro	Asn	Ala	Thr	Asn	Leu	Arg	Met	Ala	Asp	Thr	Gly	Leu	Gly	Phe	
		390					395					400				
ggc	aag	gcc	cgc	tcc	acg	ggt	gac	gtc	gag	cgt	gcg	ctg	cac	cgg	tcg	2204
Gly	Lys	Ala	Arg	Ser	Thr	Gly	Asp	Val	Glu	Arg	Ala	Leu	His	Arg	Ser	
	405					410					415					
cag	ggc	atg	ccg	tgg	gtg	aac	acg	atc	gcg	gag	gac	cgg	gag	ggt	cgc	2252
Gln	Gly	Met	Pro	Trp	Val	Asn	Thr	Ile	Ala	Ala	Asp	Arg	Ala	Gly	Arg	
420					425				430						435	
tcg	ttc	ttc	gcg	cag	tcg	cag	gtg	ctg	ccg	agg	atc	acc	gac	gcg	ttg	2300
Ser	Phe	Phe	Ala	Gln	Ser	Gln	Val	Leu	Pro	Arg	Ile	Thr	Asp	Ala	Leu	
				440					445					450		
gcg	gag	cgc	tgc	tcg	acc	ccg	ctg	ggc	cgg	gcc	acc	tac	ccc	gct	tcc	2348
Ala	Glu	Arg	Cys	Ser	Thr	Pro	Leu	Gly	Arg	Ala	Thr	Tyr	Pro	Ala	Ser	
			455					460					465			
ggc	ctc	gcg	gtg	ctg	gac	ggt	tcg	cgg	acg	gac	tgc	gag	ctg	ggc	agc	2396
Gly	Leu	Ala	Val	Leu	Asp	Gly	Ser	Arg	Thr	Asp	Cys	Ala	Leu	Gly	Ser	
		470				475					480					
gac	ccg	gac	gcg	gtg	cgg	ccg	ggg	atc	ttc	ggc	ccg	ggc	cgg	atg	ccg	2444
Asp	Pro	Asp	Ala	Val	Arg	Pro	Gly	Ile	Phe	Gly	Pro	Gly	Arg	Met	Pro	
	485					490					495					
gtg	ctg	aag	aac	cag	ccg	tac	gtg	gag	aac	tcc	aac	gac	agc	gcg	tgg	2492
Val	Leu	Lys	Asn	Gln	Pro	Tyr	Val	Glu	Asn	Ser	Asn	Asp	Ser	Ala	Trp	
500					505					510					515	
ctg	acc	aat	gcg	gag	cgg	ccg	ctg	acc	ggg	tac	gag	cgg	gtc	ttc	ggc	2540
Leu	Thr	Asn	Ala	Glu	Arg	Pro	Leu	Thr	Gly	Tyr	Glu	Arg	Val	Phe	Gly	
				520					525					530		
acg	atc	gcg	acg	ccc	cgg	tcg	atg	cgg	acg	cgc	ggc	gag	atc	gag	gac	2588
Thr	Ile	Ala	Thr	Pro	Arg	Ser	Met	Arg	Thr	Arg	Gly	Ala	Ile	Glu	Asp	
			535					540					545			

217770US0PCT.ST25

gtc	gcg	tcg	atg	gcg	gac	cgg	ggc	cgc	ctc	cgg	gtc	ggg	gac	ctt	cag	2636
Val	Ala	Ser	Met	Ala	Asp	Arg	Gly	Arg	Leu	Arg	Val	Gly	Asp	Leu	Gln	
		550					555					560				
cgg	cag	cag	ttc	gcc	aac	cgt	gcg	ccg	gcc	ggg	gat	ctg	gcc	gcc	tcc	2684
Arg	Gln	Gln	Phe	Ala	Asn	Arg	Ala	Pro	Ala	Gly	Asp	Leu	Ala	Ala	Ser	
	565					570					575					
gag	gcc	gcc	aag	tgg	tgt	gcg	gcg	ctg	ccg	ggc	ggc	acg	gcc	gtg	ggc	2732
Glu	Ala	Ala	Lys	Trp	Cys	Ala	Ala	Leu	Pro	Gly	Gly	Thr	Ala	Val	Gly	
580					585					590					595	
tcc	gac	gga	acg	ccg	gtc	gac	gtg	tcg	gcg	gcc	tgc	cgg	gtg	ctg	cgg	2780
Ser	Asp	Gly	Thr	Pro	Val	Asp	Val	Ser	Ala	Ala	Cys	Arg	Val	Leu	Arg	
				600					605					610		
cgc	tgg	gac	cgg	acc	gtg	gac	agc	gac	agc	cgg	ggc	gcg	ctg	ctc	ttc	2828
Arg	Trp	Asp	Arg	Thr	Val	Asp	Ser	Asp	Ser	Arg	Gly	Ala	Leu	Leu	Phe	
			615					620					625			
gac	cgg	ttc	tgg	cgg	aag	gcg	tcg	tcg	gcg	ccc	gcc	gcc	gag	ctg	tgg	2876
Asp	Arg	Phe	Trp	Arg	Lys	Ala	Ser	Ser	Ala	Pro	Ala	Ala	Glu	Leu	Trp	
		630					635					640				
agg	acg	ccg	ttc	gat	ccg	gcc	gac	ccg	gtg	cgc	act	ccg	cgc	ggc	ctg	2924
Arg	Thr	Pro	Phe	Asp	Pro	Ala	Asp	Pro	Val	Arg	Thr	Pro	Arg	Gly	Leu	
	645					650					655					
aac	acg	gcc	gcg	ccc	gtc	ctg	ggc	agg	gcc	ctg	gcg	gac	gcc	gtg	gcg	2972
Asn	Thr	Ala	Ala	Pro	Val	Leu	Gly	Arg	Ala	Leu	Ala	Asp	Ala	Val	Ala	
660					665					670					675	
gag	ctg	cgg	gcg	gcg	ggc	atc	gcg	ctg	gac	gcc	ccg	ctg	ggc	gag	cac	3020
Glu	Leu	Arg	Ala	Ala	Gly	Ile	Ala	Leu	Asp	Ala	Pro	Leu	Gly	Glu	His	
				680					685					690		
cag	ttc	gtc	gtg	cgg	aac	ggc	aag	cgg	ctc	ccg	atc	ggc	ggc	ggg	acg	3068
Gln	Phe	Val	Val	Arg	Asn	Gly	Lys	Arg	Leu	Pro	Ile	Gly	Gly	Gly	Thr	
			695					700					705			
gag	tcg	ctg	ggc	atc	tgg	aac	aag	acc	gag	ccg	cag	tgg	aac	gcg	gcg	3116
Glu	Ser	Leu	Gly	Ile	Trp	Asn	Lys	Thr	Glu	Pro	Gln	Trp	Asn	Ala	Ala	
		710				715						720				
ggc	ggc	ggc	tat	acg	gag	gtg	tcg	tcg	ggc	tcc	agc	tac	atc	cag	gcg	3164
Gly	Gly	Gly	Tyr	Thr	Glu	Val	Ser	Ser	Gly	Ser	Ser	Tyr	Ile	Gln	Ala	
	725					730					735					
gtc	ggc	tgg	gac	gac	agc	cgc	tgc	ccg	gtg	gcc	cgg	acg	ctg	ctg	acg	3212
Val	Gly	Trp	Asp	Asp	Ser	Arg	Cys	Pro	Val	Ala	Arg	Thr	Leu	Leu	Thr	
740					745					750					755	
tac	tcc	cag	tcg	gag	aac	ccg	aag	tca	ccg	cac	tac	agc	gac	cag	acc	3260
Tyr	Ser	Gln	Ser	Glu	Asn	Pro	Lys	Ser	Pro	His	Tyr	Ser	Asp	Gln	Thr	
				760					765					770		
agg	ctg	tac	gcg	ggt	gag	cgc	tgg	gtg	acg	tcc	cgg	ttc	tgc	gag	agg	3308
Arg	Leu	Tyr	Ala	Gly	Glu	Arg	Trp	Val	Thr	Ser	Arg	Phe	Cys	Glu	Arg	
			775					780					785			
gac	atc	gcg	cgt	tcg	ccg	gac	ctg	cgg	gtg	gtg	cgg	gtg	cac	gag	cgg	3356
Asp	Ile	Ala	Arg	Ser	Pro	Asp	Leu	Arg	Val	Val	Arg	Val	His	Glu	Arg	
		790					795					800				
cgg	tag	cgcggtg	ggc	ggacggg	ccc	gccc	atccgc	ggcgaga	aagg	gcgtccgc	cct					3412
Arg																

217770US0PCT.ST25

cggcgggagc	ccttctcacc	gatgtgtcgt	gaccgcgctc	ccgggggagc	cctcaccgag	3472
ccgccgaagg	gcccggcggc	cgaacccgtg	accatgcgtg	cgacgcatca	cgctccgctg	3532
gctccgccct	ccgcccgcgc	ccaggccagc	tgcgcgctgc	tcagcggcgg	gtcgaagcct	3592
tccgggaaca	gcagcatccg	cggctgcggc	cacatgttct	ccggtccgtg	ttcctgacag	3652
tccagggcga	ggagatgcgg	cccgtccccg	caggactcgt	gccggtaggg	gcggtcgtgc	3712
gcccggcaga	aatagccgaa	caccgcacag	tggtcgtcgc	cgcccggctg	gtggaagccg	3772
gggtcgtga	cgatcacggt	caccggctcc	tgccggttga	gccgagggat	gggccgggga	3832
tcacgccaca	acagtcgagg	agggagcaca	cgctcatctt	ccccggggcc	gagcccacgg	3892
gaagggggag	cacggcgggg	cgcctcccgt	cggcgtgatc	gaccggggcc	tcccgtcgc	3952
gggcggggcc	tcccggaccc	gttgctctac	agcgggcgct	cgaagccctc	ccagtacggt	4012
tcgcgcagcc	gccgtttgta	gagcttgccg	ttggggctgc	ggggcatggc	ggtgatgaag	4072
tcgaggctcc	ggggtcgttt	gtagccggcg	agccgctcct	cgcagtgggc	gaggatcgcg	4132
gcggcgagcg	cgggtgacgg	ctcgtggcca	tcggccgggt	cgacgacggc	cttgacctcc	4192
tcgccgcggt	cggcgtgggg	gatgccgaag	gcggcggcgt	ccgcgacggc	gggggtgggtg	4252
agcaggaccg	actcgatctc	ggcggggtag	atgttgacct	cgcccgcgat	gatcatgtcg	4312
atcttgcggt	cgcgagggaa	gaggtagccg	tcctcgtcca	gcacgccgag	gtcaccgacg	4372
gtgaagaagt	cgccgatgcg	gttcgtgcgg	gtcttggtct	cgtccttggt	gtagctgaag	4432
ccgccggtgc	tcatcttcat	gtagacgggt	cccagttcgc	ctggcgggag	gcggttgccg	4492
tcgtcgtcga	agacggccag	ttcgtgatc	ggccaggcct	tgccgacggt	gccgggcttc	4552
ttcagccagt	cctcggcggt	ggcgaacgct	ccccgcct	cgctggccgc	gtagtactcc	4612
tcgacgcagc	tccccacca	gtcgatcatg	gcgcgtttga	cgtggtcggg	gcagggggct	4672
gccccgtgga	tggcgtgccg	catggaggag	acgtcgtagc	gggacctcac	ctcgtcgggc	4732
agcgcgagca	gccggtggaa	ctgggtgggg	accatgtggg	tgtgggtgca	gcggtgggcg	4792
tcgacgaggc	gcagcatctc	ctcgggcgac	cagccgtcca	tcaggaccag	cgggtggccg	4852
atgtgcaggg	cggcgcccg	gaattggagt	acggcggtgt	ggtagagcgg	cgagcagacc	4912
aggtggacgt	tgctcgtcga	cggccggatg	ccgaagatgc	cgaggaacct	gccgaggtag	4972
gtctcctcgg	ggcgtttgcc	gggcaggggg	cgccggatgc	cgcgggggcg	gccggtgggt	5032
cccagaggtg	agttcatgac	ccagccgagg	gtgcggttct	caggcggcgt	ggcggggtgg	5092
ccttcgagga	gttcggccca	ggggcggcag	ccggggaccg	tgccgacgcc	gtagcgggtg	5152
gtcgcgggca	gttccgcctc	gtcggcgggc	gccgtcgcgg	tgcccgcgaa	gcgttcgtgg	5212
gcgatcagga	cgcgggcgcc	ggagtcggcg	acgatccagg	cgatctcggg	gccgacgagg	5272
tggtggttga	ccggcacgag	gtagaagccg	gcctgcgagg	cggcgagggt	ggcggtaggg	5332
agttcgacgc	cgttgggcag	gacgacggcg	aacgcgtcgc	cctcgcgcag	tccggccgcg	5392
cgcaggccgt	ggaccatgcg	gttgacgtcg	gcgtgcaggc	ggcccgcgct	ccactcctcg	5452

217770USOPCT.ST25

ccgtcggggg cgatcaggac ggtgcggtcg gggtcggctg cggcctgggc ccagaaaccg 5512
 ttgggcggct gggtcacgtg gcactccttc cggcgatgcg gttcatgcgg gtgacggccc 5572
 gttcgaagcc gcgggtcagg tcgtcgacga cggcccggac gctgcgttca ctggtcatcc 5632
 ggccgacgat ctgcccgcgc ggcgtgccga gcagctcgcc gacctcgtae ttctggatcc 5692

<210> 2
 <211> 804
 <212> PRT
 <213> Streptomyces Sp.

<400> 2

Leu Thr Leu Arg Asn Arg Leu Arg Leu Leu Gly Val Ala Gly Leu Ala
 1 5 10 15

Leu Phe Thr Val Ser Ala Ser Leu Pro Pro Ala Thr Ala Ser Gly Thr
 20 25 30

Gln Glu Thr Arg His Pro Ser Gly Ser Gly Leu Ser Ala Val Ile Arg
 35 40 45

Tyr Thr Glu Tyr Gly Ile Pro His Ile Val Ala Glu Asp Tyr Ala Gln
 50 55 60

Leu Gly Phe Gly Thr Gly Trp Ala Gln Ala Ala Asp Gln Val Cys Thr
 65 70 75 80

Leu Ala Asp Gly Phe Leu Thr Val Arg Gly Glu Arg Ser Arg Phe Phe
 85 90 95

Gly Pro Asp Ala Ala Thr Asp Tyr Ser Leu Ser Ser Ala Ala Thr Asn
 100 105 110

Leu Ser Ser Asp Leu Tyr Phe Arg Gly Val Arg Asp Ser Gly Thr Val
 115 120 125

Glu Lys Leu Leu Lys Glu Pro Ala Pro Ala Gly Pro Ser Arg Asp Val
 130 135 140

Lys Glu Thr Met Arg Gly Phe Ala Ala Gly Tyr Asn Ala Trp Ile Ala
 145 150 155 160

Gln Asn Arg Ile Thr Asp Pro Ala Cys Arg Gly Ala Ser Trp Val Arg
 165 170 175

Pro Val Thr Ala Leu Asp Val Ala Ala Arg Gly Tyr Ala Leu Ala Val
 180 185 190

Leu Gly Gly Gln Gly Arg Gly Ile Asp Gly Ile Thr Ala Ala Gln Pro
 195 200 205

217770US0PCT.ST25

Pro Thr Ala Ala Pro Pro Ala Ala Gly Val Thr Pro Glu Glu Ala Ala
 210 215 220
 Thr Ala Ala Glu Arg Leu Leu Ser Thr Gln Asn Ala Asp Met Gly Ser
 225 230 235 240
 Asn Ala Val Ala Phe Asp Gly Ser Thr Thr Val Asn Gly Arg Gly Leu
 245 250 255
 Leu Leu Gly Asn Pro His Tyr Pro Trp Gln Gly Gly Arg Arg Phe Trp
 260 265 270
 Gln Ala Gln Gln Thr Ile Pro Gly Glu Leu Asn Val Ser Gly Ala Ser
 275 280 285
 Leu Leu Gly Ala Thr Thr Ile Ser Ile Gly His Asn Ala Asp Val Ala
 290 295 300
 Trp Ser His Thr Val Ala Thr Gly Val Thr Leu Asn Leu His Gln Leu
 305 310 315 320
 Ser Leu Asp Pro Ala Asp Pro Thr Val Tyr Leu Val Asp Gly Lys Arg
 325 330 335
 Glu Arg Met Thr Gln Arg Thr Val Ser Val Pro Val Lys Gly Gly Ala
 340 345 350
 Asp Val Thr Arg Thr Gln Trp Trp Thr Arg Tyr Gly Pro Val Ala Thr
 355 360 365
 Ser Met Gly Ala Gly Leu Pro Leu Pro Trp Thr Ala Ser Thr Ala Tyr
 370 375 380
 Ala Leu Asn Asp Pro Asn Ala Thr Asn Leu Arg Met Ala Asp Thr Gly
 385 390 395 400
 Leu Gly Phe Gly Lys Ala Arg Ser Thr Gly Asp Val Glu Arg Ala Leu
 405 410 415
 His Arg Ser Gln Gly Met Pro Trp Val Asn Thr Ile Ala Ala Asp Arg
 420 425 430
 Ala Gly Arg Ser Phe Phe Ala Gln Ser Gln Val Leu Pro Arg Ile Thr
 435 440 445
 Asp Ala Leu Ala Glu Arg Cys Ser Thr Pro Leu Gly Arg Ala Thr Tyr
 450 455 460
 Pro Ala Ser Gly Leu Ala Val Leu Asp Gly Ser Arg Thr Asp Cys Ala
 465 470 475 480

217770USOPCT.ST25

Leu Gly Ser Asp Pro Asp Ala Val Arg Pro Gly Ile Phe Gly Pro Gly
 485 490 495
 Arg Met Pro Val Leu Lys Asn Gln Pro Tyr Val Glu Asn Ser Asn Asp
 500 505 510
 Ser Ala Trp Leu Thr Asn Ala Glu Arg Pro Leu Thr Gly Tyr Glu Arg
 515 520 525
 Val Phe Gly Thr Ile Ala Thr Pro Arg Ser Met Arg Thr Arg Gly Ala
 530 535 540
 Ile Glu Asp Val Ala Ser Met Ala Asp Arg Gly Arg Leu Arg Val Gly
 545 550 555 560
 Asp Leu Gln Arg Gln Gln Phe Ala Asn Arg Ala Pro Ala Gly Asp Leu
 565 570 575
 Ala Ala Ser Glu Ala Ala Lys Trp Cys Ala Ala Leu Pro Gly Gly Thr
 580 585 590
 Ala Val Gly Ser Asp Gly Thr Pro Val Asp Val Ser Ala Ala Cys Arg
 595 600 605
 Val Leu Arg Arg Trp Asp Arg Thr Val Asp Ser Asp Ser Arg Gly Ala
 610 615 620
 Leu Leu Phe Asp Arg Phe Trp Arg Lys Ala Ser Ser Ala Pro Ala Ala
 625 630 635 640
 Glu Leu Trp Arg Thr Pro Phe Asp Pro Ala Asp Pro Val Arg Thr Pro
 645 650 655
 Arg Gly Leu Asn Thr Ala Ala Pro Val Leu Gly Arg Ala Leu Ala Asp
 660 665 670
 Ala Val Ala Glu Leu Arg Ala Ala Gly Ile Ala Leu Asp Ala Pro Leu
 675 680 685
 Gly Glu His Gln Phe Val Val Arg Asn Gly Lys Arg Leu Pro Ile Gly
 690 695 700
 Gly Gly Thr Glu Ser Leu Gly Ile Trp Asn Lys Thr Glu Pro Gln Trp
 705 710 715 720
 Asn Ala Ala Gly Gly Gly Tyr Thr Glu Val Ser Ser Gly Ser Ser Tyr
 725 730 735
 Ile Gln Ala Val Gly Trp Asp Asp Ser Arg Cys Pro Val Ala Arg Thr
 740 745 750

217770US0PCT.ST25

Leu Leu Thr Tyr Ser Gln Ser Glu Asn Pro Lys Ser Pro His Tyr Ser
755 760 765

Asp Gln Thr Arg Leu Tyr Ala Gly Glu Arg Trp Val Thr Ser Arg Phe
770 775 780

Cys Glu Arg Asp Ile Ala Arg Ser Pro Asp Leu Arg Val Val Arg Val
785 790 795 800

His Glu Arg Arg

<210> 3
<211> 20
<212> PRT
<213> Streptomyces Sp.

<400> 3

Ser Asn Ala Val Ala Phe Asp Gly Ser Thr Thr Val Asn Gly Arg Gly
1 5 10 15

Leu Leu Leu Gly
20

<210> 4
<211> 20
<212> PRT
<213> Streptomyces Sp.

<400> 4

Gly Ser Gly Leu Ser Ala Val Ile Arg Tyr Thr Glu Tyr Gly Ile Pro
1 5 10 15

His Ile Val Ala
20

<210> 5
<211> 20
<212> PRT
<213> Streptomyces Sp.

<400> 5

Gly Ser Gly Leu Ser Ala Val Ile Arg Tyr Thr Glu Tyr Gly Ile Pro
1 5 10 15

His His Val Ala
20

<210> 6
<211> 15
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide
 <400> 6
 ctstcsgcsg tsatc 15

 <210> 7
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 7
 gtggtgsggg atsc 15

 <210> 8
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 8
 csgtsgcstt cgacgg 16

 <210> 9
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 9
 sccsagsags agscc 15

 <210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 10
 atccggtaca cgagtagcg 20

 <210> 11
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 11
 cgttcaccgt cgtggagcc 19

 <210> 12
 <211> 10

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 12
 aattgagctc 10

<210> 13
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 13
 caactgcgcg tagtcc 16

<210> 14
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 14
 catgggttcc aacgcg 16

<210> 15
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 15
 gctgtcaacc gtctgg 16

<210> 16
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 16
 acgcgctgaa cgatcc 16

<210> 17
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 17
 cggacctgga cctacc 16

<210> 18
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 18
 gtgggtgaac acgatcg 17

<210> 19
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 19
 gaccttcagc ggcagc 16

<210> 20
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 20
 caagtgggtg gcggcg 16

<210> 21
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 21
 gtcgctgggc atctgg 16

<210> 22
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 22
 gctgctgacg tactcc 16

<210> 23
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> synthetic oligonucleotide

<400> 23

gtcaaccgca tgggcc

16

<210> 24

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 24

atcgccctgga tcgtcg

16

<210> 25

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 25

cgtcagcgcg atcacc

16

<210> 26

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 26

ggtgtacagc agctgc

16

<210> 27

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 27

ctccctcgct ctgacc

16

<210> 28

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 28

gagttgtgcg cgtagg

16

<210> 29

<211> 16

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 29
 tgacgcttgg ccgtcc 16

<210> 30
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 30
 gactacgcgc agttgg 16

<210> 31
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 31
 tacaacgcgt ggatcg 16

<210> 32
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 32
 ggtgatccgg ttctgc 16

<210> 33
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 33
 gggtagtgcg ggttgc 16

<210> 34
 <211> 16
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic oligonucleotide
 <400> 34
 ctgcatcagc tcagcc 16

<210> 35
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 35
 gtccaccact gggtgc 16

<210> 36
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 36
 gaagcggggt aggtgg 16

<210> 37
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 37
 ccggtgctga agaacc 16

<210> 38
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 38
 ctgccgctga aggtcc 16

<210> 39
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 39
 tcgaacggcg tcctcc 16

<210> 40
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> synthetic oligonucleotide
 <400> 40
 tggaggacgc cgttcg 16

 <210> 41
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 41
 gcctggatgt agctgg 16

 <210> 42
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 42
 ggacatcgcg cgttcg 16

 <210> 43
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 43
 cgaacgcgcg atgtcc 16

 <210> 44
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 44
 ccgtgaccat gcgtgc 16

 <210> 45
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide
 <400> 45
 gcacgcatgg tcacgg 16

 <210> 46
 <211> 16

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 46
 gaggagacct acctcg 16

<210> 47
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 47
 aggtcccgct acgacg 16

<210> 48
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 48
 gaccatgcgg ttgacg 16

<210> 49
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 49
 cagttccgcc tcgtcg 16

<210> 50
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 50
 caggtggacg ttgtcg 16

<210> 51
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide

 <400> 51
 gtcgctgacg atcacg 16